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Sequence Listing was accepted.

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Reviewer: Keisha Douglas

Timestamp: [year=2008; month=11; day=12; hr=14; min=57; sec=12; ms=695;
]

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Application No: 10693030

Version No: 2.0

Input Set:

Output Set:

Started: 2008-10-14 16:16:37.023

Finished: 2008-10-14 16:16:38.011

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 988 ms

Total Warnings: 12

Total Errors: 0

No. of SeqIDs Defined: 12

Actual SeqID Count: 12

Error code	Error Description
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SEQUENCE LISTING

<110> KRAUS, Matthias
AARONSON, Stuart A.

<120> METHODS FOR DIAGNOSIS OF CANCER USING
erbB-3

<130> 14014.0306U2

<140> 10693030

<141> 2003-10-24

<150> 09/170,699

<151> 1998-10-13

<150> 08/473,119

<151> 1995-06-07

<150> 07/978,895

<151> 1992-11-10

<150> 07/444,406

<151> 1989-12-10

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1542

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 1

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acgtgctact caagtcaccc agtcagggtt aggtggcaga ttttgggtgtg gctgacctgc 180
tgccctcctga tgataagcag ctgctataca gtgaggccaa ggtgaggaga cacaaagggt 240
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ttcagagggc aacaaagaaa ataatgatca agaacttggg actggccggg cgcggtggct 420
cacgcctgta atcccaacac ttcgggaggg caaggcgggt ggatcacaa gtcaggagat 480
caagaccatc ctggctagca cgggtgaaacc ccgtctctac taaatataca aaaaaaaaaa 540
aattagccag gcgtggcggc atgcatctgt actcccagct actcgggagg ctgaggcagg 600
agaatggcgt gaaccagga ggcggagctt gcagtgggcc gagatcgac cactgcactc 660
cagtctgggc gacagagcga gactccgtct caaaaaaaaa aaaaaaagaa tttgggactt 720
ggaaatccta agaaaatttg tggaaataaa cttgtgatac ctctatcttt aatccgcaga 780
ctccaattaa gtggatggcc cttgagagta tccactttgg gaaatacaca caccagagt 840
atgtctggag ctatggtcag tgcactctga tgcctctct accatcactg gcccagttt 900
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tatgcagggc tacgattggc tgaagtacca gacctgctag agaaggggga gcggttgga 1140
cagccccaga tctgcacaat tgatgtctac atggatgatgg tcaagtgtga gttacctgct 1200
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gccaggctgg tctcaaactc ctgacctcag gtgatccgcc tgctcagct tcccaaagtg 1500
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<210> 2

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 2

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Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val Gln Val Ala Asp
 20             25             30
Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys Gln Leu Leu Tyr
 35             40             45
Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu Glu Ser Ile His
 50             55             60
Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr
 65             70             75             80
Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Thr Ala Gly Leu Arg
 85             90             95
Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Ala Gln
100             105             110
Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met Val Lys
115             120             125

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<210> 3

<211> 4905

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 3

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cagggtgctgg gcttgctttt cagcctggcc cggggctccg aggtgggcaa ctctcaggca 180
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acactgtaca agctctacga gaggtgtgag gtggatgatgg ggaaccttga gattgtgtct 300
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ctcgtggcca tgaatgaatt ctctactcta ccattgccca acctccgcgt ggtgcgaggg 420
accagggtct acgatgggaa gtttgccatc ttcgtcatgt tgaactataa caccaactcc 480

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agggaccgag	atgctgagat	agtgggtgaag	gacaatggca	gaagctgtcc	cccctgtcat	660
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ctccaggaga	aagtgtcaat	gtgtagaagc	cggagcagga	gccggagccc	acggccacgc	3480
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ccacccgggt	tagaggaaga	ggatgtcaac	ggttatgtca	tgccagatac	acacctcaaa	3600
ggtactccct	cctcccgga	aggcaccctt	tcttcagtg	gtcttagttc	tgtcctgggt	3660
actgaagaag	aagatgaaga	tgaggagtat	gaatacatga	accggaggag	aaggcacagt	3720
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<211> 1342

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 4

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Ala Arg Gly Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr
 20          25          30
Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
 35          40          45
Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
 50          55          60
Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
 65          70          75          80
Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
 85          90          95
Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
100         105         110
Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
115         120         125
His Ala Leu Arg Gly Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
130         135         140
Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
145         150         155         160
Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
165         170         175
Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly
180         185         190
Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr
195         200         205
Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn
210         215         220
Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp

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		260							265					270	
Glu	Pro	Asn	Pro	His	Thr	Lys	Tyr	Gln	Tyr	Gly	Gly	Val	Cys	Val	Ala
		275							280					285	
Ser	Cys	Pro	His	Asn	Phe	Val	Val	Asp	Gln	Thr	Ser	Cys	Val	Arg	Ala
		290							295					300	
Cys	Pro	Pro	Asp	Lys	Met	Glu	Val	Asp	Lys	Asn	Gly	Leu	Lys	Met	Cys
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Glu	Pro	Cys	Gly	Gly	Leu	Cys	Pro	Lys	Ala	Cys	Glu	Gly	Thr	Gly	Ser
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Gly	Ser	Arg	Phe	Gln	Thr	Val	Asp	Ser	Ser	Asn	Ile	Asp	Gly	Phe	Val
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Asn	Cys	Thr	Lys	Ile	Leu	Gly	Asn	Leu	Asp	Phe	Leu	Ile	Thr	Gly	Leu
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Asn	Gly	Asp	Pro	Trp	His	Lys	Ile	Pro	Ala	Leu	Asp	Pro	Glu	Lys	Leu
		370							375					380	
Asn	Val	Phe	Arg	Thr	Val	Arg	Glu	Ile	Thr	Gly	Tyr	Leu	Asn	Ile	Gln
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Ser	Trp	Pro	Pro	His	Met	His	Asn	Phe	Ser	Val	Phe	Ser	Asn	Leu	Thr
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Thr	Ile	Gly	Gly	Arg	Ser	Leu	Tyr	Asn	Arg	Gly	Phe	Ser	Leu	Leu	Ile
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Met	Lys	Asn	Leu	Asn	Val	Thr	Ser	Leu	Gly	Phe	Arg	Ser	Leu	Lys	Glu
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Ile	Ser	Ala	Gly	Arg	Ile	Tyr	Ile	Ser	Ala	Asn	Arg	Gln	Leu	Cys	Tyr
		450							455					460	
His	His	Ser	Leu	Asn	Trp	Thr	Lys	Val	Leu	Arg	Gly	Pro	Thr	Glu	Glu
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Gly	Lys	Val	Cys	Asp	Pro	Leu	Cys	Ser	Ser	Gly	Gly	Cys	Trp	Gly	Pro
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Gly	Pro	Gly	Gln	Cys	Leu	Ser	Cys	Arg	Asn	Tyr	Ser	Arg	Gly	Gly	Val
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Cys	Val	Thr	His	Cys	Asn	Phe	Leu	Asn	Gly	Glu	Pro	Arg	Glu	Phe	Ala
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His	Glu	Ala	Glu	Cys	Phe	Ser	Cys	His	Pro	Glu	Cys	Gln	Pro	Met	Glu
545					550					555					560
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Ala	His	Phe	Arg	Asp	Gly	Pro	His	Cys	Val	Ser	Ser	Cys	Pro	His	Gly
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Val	Leu	Gly	Ala	Lys	Gly	Pro	Ile	Tyr	Lys	Tyr	Pro	Asp	Val	Gln	Asn
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Glu	Cys	Arg	Pro	Cys	His	Glu	Asn	Cys	Thr	Gln	Gly	Cys	Lys	Gly	Pro
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Glu	Leu	Gln	Asp	Cys	Leu	Gly	Gln	Thr	Leu	Val	Leu	Ile	Gly	Lys	Thr
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His	Leu	Thr	Met	Ala	Leu	Thr	Val	Ile	Ala	Gly	Leu	Val	Val	Ile	Phe
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Met	Met	Leu	Gly	Gly	Thr	Phe	Leu	Tyr	Trp	Arg	Gly	Arg	Arg	Ile	Gln
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Asn	Lys	Arg	Ala	Met	Arg	Arg	Tyr	Leu	Glu	Arg	Gly	Glu	Ser	Ile	Glu
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Pro	Leu	Asp	Pro	Ser	Glu	Lys	Ala	Asn	Lys	Val	Leu	Ala	Arg	Ile	Phe	690	695	700
Lys	Glu	Thr	Glu	Leu	Arg	Lys	Leu	Lys	Val	Leu	Gly	Ser	Gly	Val	Phe	705	710	715
Gly	Thr	Val	His	Lys	Gly	Val	Trp	Ile	Pro	Glu	Gly	Glu	Ser	Ile	Lys	725	730	735
Ile	Pro	Val	Cys	Ile	Lys	Val	Ile	Glu	Asp	Lys	Ser	Gly	Arg	Gln	Ser	740	745	750
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Ala	His	Ile	Val	Arg	Leu	Leu	Gly	Leu	Cys	Pro	Gly	Ser	Ser	Leu	Gln	770	775	780
Leu	Val	Thr	Gln	Tyr	Leu	Pro	Leu	Gly	Ser	Leu	Leu	Asp	His	Val	Arg	785	790	795
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Gln	Ile	Ala	Lys	Gly	Met	Tyr	Tyr	Leu	Glu	Glu	His	Gly	Met	Val	His	820	825	830
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Gln	Val	Ala	Asp	Phe	Gly	Val	Ala	Asp	Leu	Leu	Pro	Pro	Asp	Asp	Lys	850	855	860
Gln	Leu	Leu	Tyr	Ser	Glu	Ala	Lys	Thr	Pro	Ile	Lys	Trp	Met	Ala	Leu	865	870	875
Glu	Ser	Ile	His	Phe	Gly	Lys	Tyr	Thr	His	Gln	Ser	Asp	Val	Trp	Ser	885	890	895
Tyr	Gly	Val	Thr	Val	Trp	Glu	Leu	Met	Thr	Phe	Gly	Ala	Glu	Pro	Tyr	900	905	910
Ala	Gly	Leu	Arg	Leu	Ala	Glu	Val	Pro	Asp	Leu	Leu	Glu	Lys	Gly	Glu	915	920	925
Arg	Leu	Ala	Gln	Pro	Gln	Ile	Cys	Thr	Ile	Asp	Val	Tyr	Met	Val	Met	930	935	940
Val	Lys	Cys	Trp	Met	Ile	Asp	Glu	Asn	Ile	Arg	Pro	Thr	Phe	Lys	Glu	945	950	955
Leu	Ala	Asn	Glu	Phe	Thr	Arg	Met	Ala	Arg	Asp	Pro	Pro	Arg	Tyr	Leu	965	970	975
Val	Ile																	